Amendments to the Specification:

Please replace the paragraph [0023] with the following amended paragraph:

[0023] FIG. 8 displays an HPLC chromatogram of peptide containing a cysteic acid residue eluding at approximately 24 minutes (LRRA(cysteic acid)LG) (SEQ ID NO:1)and the digested peptide fragments after cleavage with Asp-N eluting at approximately 20 minutes (LRRA) (SEQ ID NO:2) and approximately 12 minutes ((cysteic acid)LG)..

Please replace the paragraph [0024] with the following amended paragraph:

[0024] FIG. 9 (A) reaction scheme demonstrating the conversion of phosphothreonine to β-methyl aminoethylcysteine. (B) MALDI-MS spectrum of Lys-C peptidase digested β-methyl aminoethylcysteine modified peptide having the sequence ZFRP (β-methyl aminoethylcysteine) as shown at m/z 698.4, with the undigested β-methyl aminoethylcysteine modified peptide at m/z 1225.5 (having the sequence ZFRP(β-methyl aminoethylcysteine)GFY(Nitro)E) (SEQ ID NO:3) and the undigested phosphorylated peptide ad m/z 1246.5 (having the sequence ZFRPpTGFY(Nitro)E (SEQ ID NO:4).

Please replace the paragraph [0037] with the following amended paragraph:

[0037] FIG 22 (A) Mass spectrum of a peptide containing an aminoethylcysteine modification shown at m/z 1412.8 (NKPPR(aminoethylcysteine)PVVELSK) (SEQ ID NO:5).. (B) Mass spectrum of a peptide containing an phosphoserine with no peak at the expected m/z 1433.7 (NKPPRpSPVVELSK) (SEQ ID NO:6) and unmodified peptide NKPPRSPVVELSK = SEQ ID NO:7).

Please replace the paragraph [0038] with the following amended paragraph:

[0038] **FIG. 23** displays a mass spectrum of guanidinated MARCKS peptide after cleavage with Lys-C ($K^{gn}K^{gn}K^{gn}K^{gn}K^{gn}RFK^{*8}FK^{gn}K^{gn}K^{*12}FK^{gn}LSGFK^{*19}FK^{gn}K^{gn}NK^{gn}K^{gn}$= SEQ ID NO:8).

Please replace the paragraph [0039] with the following amended paragraph:

[0039] **FIG. 24** displays a mass spectrum of an acetylated MARCKS peptide after cleavage with Lys-C (KKKKKRFK* = SEQ ID NO:9; KKKKKRFK*FKKK* = SEQ ID NO:10; KKKKKRFK*FKKK*FKLSGFK* = SEQ ID NO:11; and KKKKKRFK*FKKK*FKLSGFK*FKKNKK = SEQ ID NO:12).

Please replace the paragraph [0040] with the following amended paragraph:

[0040] **FIG. 25** displays a mass spectrum of an acetylated MARCKS peptide after cleavage with Lys-C with the detection of the six additional predicted mass peaks (K*)FKLSGFK* = SEQ ID NO:13; (K*)FKKNKK = SEQ ID NO14; KKKKKRFK* = SEQ ID NO:9; (K*)FKKK*FKLSGFK* = SEQ ID NO:15; FKLSGFK*FKKNKK = SEQ ID NO16; KKKKKRFK*FKKK* = SEQ ID NO:10; (K*)FKKK*FKLSGFK*FKKNKK = SEQ ID NO:17; KKKKKRFK*FKKK*FKLSGFK* = SEQ ID NO:11 and KKKKKRFK*FKKK*FKLSGFK*FKKNKK = SEQ ID NO:12)

Please replace the Table 1 on page 35 with the following amended Table 1:

Table 1

Sequence	Exp. Mass (Calcd. Mass) Dehydroalanine Aminoethylcys Lys-C Digest			Seq ID No.
GRTGRRNpSIHDIL	1476.4 (1476.8)	1554.6 (1553.8)	610.4 (610.4)	(18)
DLDVPIPGRFDRRVpSVAAE	2094.0 (2094.1)	2170.6 (2171.1)	1801.0 (1801.0)	(19)
SLRRSpSC*FGGRIDRIGAQS				
GLGC*NSFRY	3141.4 (3141.5)	3218.2 (3218.5)	2472.8 (2473.1)	(20)
KRPpSQRHGSKY	1325.4 (1324.7)	1402.2 (1401.8)	712.6 (712.4)	(21)
LRRApSLG	754.6 (754.4)	831.6 (831.5)	661.4 (661.4)	(22)
ZFRPpSGFY*D	1134.7 (1134.5)	1211.7 (1211.5)	684.6 (684.3)	(23)
ZFRPpTGFY*D	1147.5 (1147.5)	1224.5(1224.5)	697.4 (697.3)	(24)
KRpTIRR	810.6(810.5)	887.6(887.6)	n/a	(25)

The symbols C* and Y* represent cysteic acid and nitrotyrosine, respectively.

Please replace the Table 2 on page 36 with the following amended Table 2:

Table 2

Protein	Residues	Peptide Sequence	Exp. Mass	Calcd. Mass	Seq ID NO:
α_{s1}-casein	43-58	DIGK*EK*TEDQAM(SO_2)EDIK	1917.75	1917.79	(26)
α_{s1}-casein	47-58	(K*)EK*TEDQAM(SO_2)EDIK	1486.54	1486.60	(27)
α_{s1}-casein	49-58	(K*)TEDQAM(SO_2)EDIK	1211.47	1211.51	(28)
α_{s1}-casein	106-119	VPQLEIVPNK*AEER	1639.85	1639.85	(29)
α_{s1}-casein	106-115	VPQLEIVPNK*	1154.59	1154.62	(30)
α_{s2}-casein	153-164	TVDMEK*TEVFTK	1477.61	1477.67	(31)
α_{s2}-casein	159-164	(K*)TEVFTK	724.37	724.39	(32)
β-casein	1-25	RELEELNVPGEIVEK*LK*K*K*EESITR	3038.40	3038.48	(33)
β-casein	1-19	RELEELNVPGEIVEK*LK*K*K*	2323.12	2323.13	(34)
β-casein	1-18	RELEELNVPGEIVEK*LK*K*	2177.04	2177.08	(35)
β-casein	1-17	RELEELNVPGEIVEK*LK*	2030.93	2031.02	(36)
β-casein	1-15	RELEELNVPGEIVEK*	1771.79	1771.89	(37)
β-casein	33-48	FQK*EEQQQTEDELQDK	2040.81	2040.88	(38)
β-casein	36-48	(K*)EEQQQTEDELQDK	1619.66	1619.70	(39)
MARCKS	1-25	ac-KKKKKRFK*FKKK*FKLSGFK*FKKNKK			(40)
MARCKS	1-19	ac-KKKKKRFK*FKKK*FKLSGFK*			(41)
MARCKS	1-12	ac-KKKKKRFK*FKKK*			(42)
MARCKS	1-8	ac-KKKKKRFK*			(43)
MARCKS	9-25	FKKK*FKLSGFK*FKKNKK			(44)
MARCKS	9-19	FKKK*FKLSGFK*			(45)
MARCKS	9-12	FKKK*			
MARCKS	13-25	FKLSGFK*FKKNKK			(16)
MARCKS	13-19	FKLSGFK*			(46)
MARCKS	20-25	(K*)FKKNKK			(47)

The symbol K* represents aminoethylcysteine.

Please replace the paragraph [0162] with the following amended paragraph:

[0162] N-terminal His6-tagged GRK2 (SEQ ID NO:48) was expressed in SF9 insect cells and purified using Ni-NTA beads (Qiagen) as described37. Bovine tubulin was a gift from Ron Vale. Tubulin (5 μM) and GRK2 (0.6 μM) were incubated in 100 μl of 20 mM HEPES, pH 7.4, 2.0 mM EDTA, 10 mM MgCl2 containing 1 mM ATP. Kinase reactions were performed at 25 °C for 3 hours22, after which the reactions were desalted by microdialysis, subjected to aminoethylcysteine modification, digested with either Lys-C/Trypsin or Lys-C/Asp-N, and finally analyzed by LC-MS/MS and MALDI-MS as described above. In a similar fashion, purified GRK2 (~5 μg) was subjected to aminoethylcysteine modification, digested with Lys-C, and then analyzed by mass spectrometry as described. **Table 3** shows the identification of serine and threonine phosphorylation sites in GRK2 and tubulin using the cysteamine chemical modification reagent. **FIG 22** illustrates the enhancement of the mass spectroscopy response of a GRK2 phosphorylation site using the cysteamine chemical modification reagent (panel A) versus no chemical modification reagent (Panel B).

Please replace the Table 3 on page 42 with the following amended Table 3:

Table 3

PROTEIN	RESIDUES	SEQUENCE	EXP. MASS	CALC. MASS	SEQ ID NO:
GRK2	666-677	NKPRK*PVVPELSK	1411.78	1411.80	49
GRK2	668-677	PRK*PVVPELSK	1169.62	1169.66	50
GRK2	671-677	K*PVVPELSK	771.40	771.45	51
β-Tubulin	404-416	DEMEFK^{T}*EASNMN	1604.52	1604.58	52
β-Tubulin	404-416	DEM**EFK^{T}*EASNMN	1620.60	1620.57	53
β-Tubulin	404-409	DEMEFK^{T}*	829.34	829.30	54
β-Tubulin	404-409	DEM**EFK^{T}*	845.38	845.30	55
β-Tubulin	417-426	DLVK*EYQQYQ	1330.51	1330.58	56

β-Tubulin	421-426	K*EYQQYQ	857.32	857.36	57
β-Tubulin	417-420	DLVK*	491.26	491.24	

The symbol M** represents methionine sulfoxide. The symbols K* and K^T* represent, aminoethylcysteine and β-methyl aminoethylcysteine, respectively.